

RAW SEQUENCE LISTING

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Application Serial Number: 10/560, 491
Source: IEWP
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RAW SEQUENCE LISTING

PATENT APPLICATION: US/10/560,491

DATE: 12/21/2005

TIME: 15:20:11

Input Set : N:\RJAVED\10560491.txt

Output Set: N:\CRF4\12212005\J560491.raw

3 <110> APPLICANT: YANASE, Michiyo
 4 TAKATA, Hiroki
 5 FUJII, Kazutoshi
 6 TAKAHA, Takeshi
 7 Kuriki, Takashi
 9 <120> TITLE OF INVENTION: A METHOD FOR IMPROVING THE THERMOSTABILITY OF ALPHA-GLUCAN
 PHOSPHORYLASE
 10 (GP)
 12 <130> FILE REFERENCE: EG012PCT
 C--> 14 <140> CURRENT APPLICATION NUMBER: US/10/560,491
 C--> 15 <141> CURRENT FILING DATE: 2005-12-12
 17 <150> PRIOR APPLICATION NUMBER: JP 2003-173972
 18 <151> PRIOR FILING DATE: 2003-06-18
 20 <160> NUMBER OF SEQ ID NOS: 48
 22 <170> SOFTWARE: PatentIn version 3.3
 24 <210> SEQ ID NO: 1
 25 <211> LENGTH: 3101
 26 <212> TYPE: DNA
 27 <213> ORGANISM: Solanum tuberosum
 30 <220> FEATURE:
 31 <221> NAME/KEY: CDS
 32 <222> LOCATION: (44)..(2941)
 34 <220> FEATURE:
 35 <221> NAME/KEY: mat_peptide
 36 <222> LOCATION: (194)..(2941)
 38 <400> SEQUENCE: 1
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 40 Met Ala Thr Ala
 41 -50
 43 aat gga gca cac ttg ttc aac cat tac agc tcc aat tcc aga ttc atc 103
 44 Asn Gly Ala His Leu Phe Asn His Tyr Ser Ser Asn Ser Arg Phe Ile
 45 -45 -40 -35
 47 cat ttc act tct aga aac aca agc tcc aaa ttg ttc ctt acc aaa acc 151
 48 His Phe Thr Ser Arg Asn Thr Ser Ser Lys Leu Phe Leu Thr Lys Thr
 49 -30 -25 -20 -15
 51 tcc cat ttt cgg aga ccc aaa cgc tgt ttc cat gtc aac aat acc ttg 199
 52 Ser His Phe Arg Arg Pro Lys Arg Cys Phe His Val Asn Asn Thr Leu
 53 -10 -5 -1 1
 55 agt gag aaa att cac cat ccc att act gaa caa ggt ggt gag agc gac 247
 56 Ser Glu Lys Ile His His Pro Ile Thr Glu Gln Gly Gly Glu Ser Asp
 57 5 10 15
 59 ctg agt tct ttt gct cct gat gcc gca tct att acc tca agt atc aaa 295
 60 Leu Ser Ser Phe Ala Pro Asp Ala Ala Ser Ile Thr Ser Ser Ile Lys
 61 20 25 30

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63 tac cat gca gaa ttc aca cct gta ttc tct cct gaa agg ttt gag ctc	343
64 Tyr His Ala Glu Phe Thr Pro Val Phe Ser Pro Glu Arg Phe Glu Leu	
65 35 40 45 50	
67 cct aag gca ttc ttt gca aca gct caa agt gtt cgt gat tcg ctc ctt	391
68 Pro Lys Ala Phe Phe Ala Thr Ala Gln Ser Val Arg Asp Ser Leu Leu	
69 55 60 65	
71 att aat tgg aat gct acg tat gat att tat gaa aag ctg aac atg aag	439
72 Ile Asn Trp Asn Ala Thr Tyr Asp Ile Tyr Glu Lys Leu Asn Met Lys	
73 70 75 80	
75 caa gcg tac tat cta tcc atg gaa ttt ctg cag ggt aga gca ttg tta	487
76 Gln Ala Tyr Tyr Leu Ser Met Glu Phe Leu Gln Gly Arg Ala Leu Leu	
77 85 90 95	
79 aat gca att ggt aat ctg gag ctt act ggt gca ttt gcg gaa gct ttg	535
80 Asn Ala Ile Gly Asn Leu Glu Leu Thr Gly Ala Phe Ala Glu Ala Leu	
81 100 105 110	
83 aaa aac ctt ggc cac aat cta gaa aat gtg gct tct cag gaa cca gat	583
84 Lys Asn Leu Gly His Asn Leu Glu Asn Val Ala Ser Gln Glu Pro Asp	
85 115 120 125 130	
87 gct gct ctt gga aat ggg ggt ttg gga cgg ctt gct tcc tgt ttt ctg	631
88 Ala Ala Leu Gly Gly Leu Gly Arg Leu Ala Ser Cys Phe Leu	
89 135 140 145	
91 gac tct ttg gca aca cta aac tac cca gca tgg ggc tat gga ctt agg	679
92 Asp Ser Leu Ala Thr Leu Asn Tyr Pro Ala Trp Gly Tyr Gly Leu Arg	
93 150 155 160	
95 tac aag tat ggt tta ttt aag caa cgg att aca aaa gat ggt cag gag	727
96 Tyr Lys Tyr Gly Leu Phe Lys Gln Arg Ile Thr Lys Asp Gly Gln Glu	
97 165 170 175	
99 gag gtg gct gaa gat tgg ctt gaa att ggc agt cca tgg gaa gtt gtg	775
100 Glu Val Ala Glu Asp Trp Leu Glu Ile Gly Ser Pro Trp Glu Val Val	
101 180 185 190	
103 agg aat gat gtt tca tat cct atc aaa ttc tat gga aaa gtc tct aca	823
104 Arg Asn Asp Val Ser Tyr Pro Ile Lys Phe Tyr Gly Lys Val Ser Thr	
105 195 200 205 210	
107 gga tca gat gga aag agg tat tgg att ggt gga gag gat ata aag gca	871
108 Gly Ser Asp Gly Lys Arg Tyr Trp Ile Gly Gly Glu Asp Ile Lys Ala	
109 215 220 225	
111 gtt gcg tat gat gtt ccc ata cca ggg tat aag acc aga acc aca atc	919
112 Val Ala Tyr Asp Val Pro Ile Pro Gly Tyr Lys Thr Arg Thr Thr Ile	
113 230 235 240	
115 agc ctt cga ctg tgg tct aca cag gtt cca tca gcg gat ttt gat tta	967
116 Ser Leu Arg Leu Trp Ser Thr Gln Val Pro Ser Ala Asp Phe Asp Leu	
117 245 250 255	
119 tct gct ttc aat gct gga gag cac acc aaa gca tgt gaa gcc caa gca	1015
120 Ser Ala Phe Asn Ala Gly Glu His Thr Lys Ala Cys Glu Ala Gln Ala	
121 260 265 270	
123 aac gct gag aag ata tgt tac ata ctc tac cct ggg gat gaa tca gag	1063
124 Asn Ala Glu Lys Ile Cys Tyr Ile Leu Tyr Pro Gly Asp Glu Ser Glu	
125 275 280 285 290	
127 gag gga aag atc ctt cgg ttg aag caa caa tat acc tta tgc tcg gct	1111

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128	Glu	Gly	Lys	Ile	Leu	Arg	Leu	Lys	Gln	Gln	Tyr	Thr	Leu	Cys	Ser	Ala	
129				295					300					305			
131	tct	ctc	caa	gat	att	att	tct	cga	ttt	gag	agg	aga	tca	ggt	gat	cgt	1159
132	Ser	Leu	Gln	Asp	Ile	Ile	Ser	Arg	Phe	Glu	Arg	Arg	Ser	Gly	Asp	Arg	
133					310				315					320			
135	att	aag	tgg	gaa	gag	ttt	cct	gaa	aaa	gtt	gct	gtg	cag	atg	aat	gac	1207
136	Ile	Lys	Trp	Glu	Glu	Phe	Pro	Glu	Lys	Val	Ala	Val	Gln	Met	Asn	Asp	
137					325				330				335				
139	act	cac	cct	aca	ctt	tgt	atc	cct	gag	ctg	atg	aga	ata	ttg	ata	gat	1255
140	Thr	His	Pro	Thr	Leu	Cys	Ile	Pro	Glu	Leu	Met	Arg	Ile	Leu	Ile	Asp	
141					340				345				350				
143	ctg	aag	ggc	ttg	aat	tgg	aat	gaa	gct	tgg	aat	att	act	caa	aga	act	1303
144	Leu	Lys	Gly	Leu	Asn	Trp	Asn	Glu	Ala	Trp	Asn	Ile	Thr	Gln	Arg	Thr	
145					355				360			365		370			
147	gtg	gcc	tac	aca	aac	cat	act	gtt	ttg	cct	gag	gca	ctg	gag	aaa	tgg	1351
148	Val	Ala	Tyr	Thr	Asn	His	Thr	Val	Leu	Pro	Glu	Ala	Leu	Glu	Lys	Trp	
149						375				380			385				
151	agt	tat	gaa	ttg	atg	cag	aaa	ctc	ctt	ccc	aga	cat	gtc	gaa	atc	att	1399
152	Ser	Tyr	Glu	Leu	Met	Gln	Lys	Leu	Leu	Pro	Arg	His	Val	Glu	Ile	Ile	
153						390				395			400				
155	gag	gcg	att	gac	gag	gag	ctg	gta	cat	gaa	att	gta	tta	aaa	tat	ggt	1447
156	Glu	Ala	Ile	Asp	Glu	Glu	Leu	Val	His	Glu	Ile	Val	Leu	Lys	Tyr	Gly	
157					405				410			415					
159	tca	atg	gat	ctg	aac	aaa	ttg	gag	gaa	aag	ttg	act	aca	atg	aga	atc	1495
160	Ser	Met	Asp	Leu	Asn	Lys	Leu	Glu	Glu	Lys	Leu	Thr	Thr	Met	Arg	Ile	
161					420				425			430					
163	tta	gaa	aat	ttt	gat	ctt	ccc	agt	tct	gtt	gct	gaa	tta	ttt	att	aag	1543
164	Leu	Glu	Asn	Phe	Asp	Leu	Pro	Ser	Ser	Val	Ala	Glu	Leu	Phe	Ile	Lys	
165					435				440			445		450			
167	cct	gaa	atc	tca	gtt	gat	gat	act	gaa	aca	gtt	gaa	gtc	cat	gac		1591
168	Pro	Glu	Ile	Ser	Val	Asp	Asp	Asp	Thr	Glu	Thr	Val	Glu	Val	His	Asp	
169						455				460			465				
171	aaa	gtt	gaa	gct	tcc	gat	aaa	gtt	gtg	act	aat	gat	gaa	gat	gac	act	1639
172	Lys	Val	Glu	Ala	Ser	Asp	Lys	Val	Val	Thr	Asn	Asp	Glu	Asp	Asp	Thr	
173						470				475			480				
175	ggt	aag	aaa	act	agt	gtg	aag	ata	gaa	gca	gct	gca	gaa	aaa	gac	att	1687
176	Gly	Lys	Lys	Thr	Ser	Val	Lys	Ile	Glu	Ala	Ala	Ala	Glu	Lys	Asp	Ile	
177						485				490			495				
179	gac	aag	aaa	act	ccc	gtg	agt	ccg	gaa	cca	gct	gtt	ata	cca	cct	aag	1735
180	Asp	Lys	Lys	Thr	Pro	Val	Ser	Pro	Glu	Pro	Ala	Val	Ile	Pro	Pro	Lys	
181						500				505			510				
183	aag	gta	cgc	atg	gcc	aac	ttg	tgt	gtt	gtg	ggc	ggc	cat	gct	gtt	aat	1783
184	Lys	Val	Arg	Met	Ala	Asn	Leu	Cys	Val	Val	Gly	Gly	His	Ala	Val	Asn	
185						515				520			525		530		
187	gga	gtt	gct	gag	atc	cat	agt	gaa	att	gtg	aag	gag	gag	gtt	ttc	aat	1831
188	Gly	Val	Ala	Glu	Ile	His	Ser	Glu	Ile	Val	Lys	Glu	Glu	Val	Phe	Asn	
189							535			540			545				
191	gac	ttc	tat	gag	ctc	tgg	ccg	gaa	aag	ttc	caa	aac	aaa	aca	aat	gga	1879
192	Asp	Phe	Tyr	Glu	Leu	Trp	Pro	Glu	Lys	Phe	Gln	Asn	Lys	Thr	Asn	Gly	

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193	550	555	560	
195	gtg act cca aga aga tgg att cgt ttc tgc aat cct cct ctt agt gcc			1927
196	Val Thr Pro Arg Arg Trp Ile Arg Phe Cys Asn Pro Pro Leu Ser Ala			
197	565	570	575	
199	atc ata act aag tgg act ggt aca gag gat tgg gtc ctg aaa act gaa			1975
200	Ile Ile Thr Lys Trp Thr Gly Thr Glu Asp Trp Val Leu Lys Thr Glu			
201	580	585	590	
203	aag ttg gca gaa ttg cag aag ttt gct gat aat gaa gat ctt caa aat			2023
204	Lys Leu Ala Glu Leu Gln Lys Phe Ala Asp Asn Glu Asp Leu Gln Asn			
205	595	600	605	610
207	gag tgg agg gaa gca aaa agg agc aac aag att aaa gtt gtc tcc ttt			2071
208	Glu Trp Arg Glu Ala Lys Arg Ser Asn Lys Ile Lys Val Val Ser Phe			
209	615	620	625	
211	ctc aaa gaa aag aca ggg tat tct gtt gtc cca gat gca atg ttt gat			2119
212	Leu Lys Glu Lys Thr Gly Tyr Ser Val Val Pro Asp Ala Met Phe Asp			
213	630	635	640	
215	att cag gta aaa cgc att cat gag tac aag cga caa ctg tta aat atc			2167
216	Ile Gln Val Lys Arg Ile His Glu Tyr Lys Arg Gln Leu Leu Asn Ile			
217	645	650	655	
219	tcc ggc atc gtt tat cgg tat aag aag atg aaa gaa atg aca gct gca			2215
220	Phe Gly Ile Val Tyr Arg Tyr Lys Lys Met Lys Glu Met Thr Ala Ala			
221	660	665	670	
223	gaa aga aag act aac ttc gtt cct cga gta tgc ata ttt ggg gga aaa			2263
224	Glu Arg Lys Thr Asn Phe Val Pro Arg Val Cys Ile Phe Gly Gly Lys			
225	675	680.	685	690
227	gct ttt gcc aca tat gtg caa gcc aag agg att gta aaa ttt atc aca			2311
228	Ala Phe Ala Thr Tyr Val Gln Ala Lys Arg Ile Val Lys Phe Ile Thr			
229	695	700	705	
231	gat gtt ggt gct act ata aat cat gat cca gaa atc ggt gat ctg ttg			2359
232	Asp Val Gly Ala Thr Ile Asn His Asp Pro Glu Ile Gly Asp Leu Leu			
233	710	715	720	
235	aag gta gtc ttt gtg cca gat tac aat gtc agt gtt gct gaa ttg cta			2407
236	Lys Val Val Phe Val Pro Asp Tyr Asn Val Ser Val Ala Glu Leu Leu			
237	725	730	735	
239	att cct gct agc gat cta tca gaa cat atc agt acg gct gga atg gag			2455
240	Ile Pro Ala Ser Asp Leu Ser Glu His Ile Ser Thr Ala Gly Met Glu			
241	740	745	750	
243	gcc agt gga acc agt aat atg aag ttt gca atg aat ggt tgt atc caa			2503
244	Ala Ser Gly Thr Ser Asn Met Lys Phe Ala Met Asn Gly Cys Ile Gln			
245	755	760	765	770
247	att ggt aca ttg gat ggc gct aat gtt gaa ata agg gaa gag gtt gga			2551
248	Ile Gly Thr Leu Asp Gly Ala Asn Val Glu Ile Arg Glu Glu Val Gly			
249	775	780	785	
251	gaa gaa aac ttc ttt ctc ttt ggt gct caa gct cat gaa att gca ggg			2599
252	Glu Glu Asn Phe Phe Leu Phe Gly Ala Gln Ala His Glu Ile Ala Gly			
253	790	795	800	
255	cgt aga aaa gaa aga gct gac gga aag ttt gta cct gat gaa cgt ttt			2647
256	Leu Arg Lys Glu Arg Ala Asp Gly Lys Phe Val Pro Asp Glu Arg Phe			
257	805	810	815	

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259	gaa	gag	gtg	aag	gaa	ttt	gtt	aga	agc	ggt	gct	ttt	ggc	tct	tat	aac	2695
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261	820				825						830						
263	tat	gat	gac	cta	att	gga	tcg	ttg	gaa	gga	aat	gaa	ggt	ttt	ggc	cgt	2743
264	Tyr	Asp	Asp	Leu	Ile	Gly	Ser	Leu	Glu	Gly	Asn	Glu	Gly	Phe	Gly	Arg	
265	835				840				845				850				
267	gct	gac	tat	ttc	ctt	gtg	ggc	aag	gac	ttc	ccc	agt	tac	ata	gaa	tgc	2791
268	Ala	Asp	Tyr	Phe	Leu	Val	Gly	Lys	Asp	Phe	Pro	Ser	Tyr	Ile	Glu	Cys	
269	855				860						865						
271	caa	gag	aaa	gtt	gat	gag	gca	tat	cgc	gac	cag	aaa	agg	tgg	aca	acg	2839
272	Gln	Glu	Lys	Val	Asp	Glu	Ala	Tyr	Arg	Asp	Gln	Lys	Arg	Trp	Thr	Thr	
273	870				875			880									
275	atg	tca	atc	ttg	aat	aca	gcg	gga	tcg	tac	aag	ttc	agc	agt	gac	aga	2887
276	Met	Ser	Ile	Leu	Asn	Thr	Ala	Gly	Ser	Tyr	Lys	Phe	Ser	Ser	Asp	Arg	
277	885				890			895									
279	aca	atc	cat	gaa	tat	gcc	aaa	gac	att	tgg	aac	att	gaa	gct	gtg	gaa	2935
280	Thr	Ile	His	Glu	Tyr	Ala	Lys	Asp	Ile	Trp	Asn	Ile	Glu	Ala	Val	Glu	
281	900				905			910									
283	ata	gca	taagaggggg	aagtgaatga	aaaataacaa	aggcacagta	agtagttct										2991
284	Ile	Ala															
285	915																
287	cttttatca	tgtgatgaag	gtatataatg	tatgtgtaag	aggatgatgt	tattaccaca											3051
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303	Ser	Arg	Phe	Ile	His	Phe	Thr	Ser	Arg	Asn	Thr	Ser	Ser	Lys	Leu	Phe	
304					-30				-25				-20				
307	Leu	Thr	Lys	Thr	Ser	His	Phe	Arg	Arg	Pro	Lys	Arg	Cys	Phe	His	Val	
308					-15			-10			-5						
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312	-1	1			5			10									
315	Gly	Glu	Ser	Asp	Leu	Ser	Ser	Phe	Ala	Pro	Asp	Ala	Ala	Ser	Ile	Thr	
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319	Ser	Ser	Ile	Lys	Tyr	His	Ala	Glu	Phe	Thr	Pro	Val	Phe	Ser	Pro	Glu	
320					35			40			45						
323	Arg	Phe	Glu	Leu	Pro	Lys	Ala	Phe	Phe	Ala	Thr	Ala	Gln	Ser	Val	Arg	
324					50			55			60						
327	Asp	Ser	Leu	Leu	Ile	Asn	Trp	Asn	Ala	Thr	Tyr	Asp	Ile	Tyr	Glu	Lys	
328					65			70			75						
331	Leu	Asn	Met	Lys	Gln	Ala	Tyr	Tyr	Leu	Ser	Met	Glu	Phe	Leu	Gln	Gly	
332					80			85			90						
335	Arg	Ala	Leu	Leu	Asn	Ala	Ile	Gly	Asn	Leu	Glu	Leu	Thr	Gly	Ala	Phe	
336	95				100					105			110				
339	Ala	Glu	Ala	Leu	Lys	Asn	Leu	Gly	His	Asn	Leu	Glu	Asn	Val	Ala	Ser	

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Invalid Line Length:

The rules require that a line not exceed 72 characters in length. This includes spaces.

Seq#:1; Line(s) 9

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L:14 M:270 C: Current Application Number differs, Replaced Current Application Number

L:15 M:271 C: Current Filing Date differs, Replaced Current Filing Date